



SEQUENCE LISTING

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Schlokat, Uwe
Baxter Aktiengesellschaft

<120> Factor X Analog With an Improved Ability to be
Activated

<130> 20695C-005700US

<140> US 09/632.722

<141> 2000-08-04

<150> AT A1377/99

<151> 1999-08-10

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 1467

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1467)

<223> factor X

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ctc ctg ctg ctc ggg gaa agt ctg ttc atc cgc agg gag cag gcc aac 96
Leu Leu Leu Leu Gly Glu Ser Leu Phe Ile Arg Arg Glu Gln Ala Asn
20 25 30

aac atc ctg gcg agg gtc acg agg gcc aat tcc ttt ctt gaa gag atg 144
Asn Ile Leu Ala Arg Val Thr Arg Ala Asn Ser Phe Leu Glu Glu Met
35 40 45

aag aaa gga cac ctc gaa aga gag tgc atg gaa gag acc tgc tca tac 192
Lys Lys Gly His Leu Glu Arg Glu Cys Met Glu Glu Thr Cys Ser Tyr
50 55 60

gaa gag gcc cgc gag gtc ttt gag gac agc gac aag acg aat gaa ttc 240
Glu Glu Ala Arg Glu Val Phe Glu Asp Ser Asp Lys Thr Asn Glu Phe
65 70 75 80

tgg aat aaa tac aaa gat ggc gac cag tgt gag acc agt cct tgc cag 288
Trp Asn Lys Tyr Lys Asp Gly Asp Gln Cys Glu Thr Ser Pro Cys Gln
85 90 95

aac cag ggc aaa tgt aaa gac ggc ctc ggg gaa tac acc tgc acc tgt 336
Asn Gln Gly Lys Cys Lys Asp Gly Leu Gly Glu Tyr Thr Cys Thr Cys
100 105 110

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TECH CENTER 1600/2900

tta gaa gga ttc gaa ggc aaa aac tgt gaa tta ttc aca cgg aag ctc	384
Leu Glu Gly Phe Glu Gly Lys Asn Cys Glu Leu Phe Thr Arg Lys Leu	
115 120 125	
tgc agc ctg gac aac ggg gac tgt gac cag ttc tgc cac gag gaa cag	432
Cys Ser Leu Asp Asn Gly Asp Cys Asp Gln Phe Cys His Glu Glu Gln	
130 135 140	
aac tct gtg gtg tgc tcc tgc gcc cgc ggg tac acc ctg gct gac aac	480
Asn Ser Val Val Cys Ser Cys Ala Arg Gly Tyr Thr Leu Ala Asp Asn	
145 150 155 160	
ggc aag gcc tgc att ccc aca ggg ccc tac ccc tgt ggg aaa cag acc	528
Gly Lys Ala Cys Ile Pro Thr Gly Pro Tyr Pro Cys Gly Lys Gln Thr	
165 170 175	
ctg gaa cgc agg aag agg tca gtg gcc cag gcc acc agc agc agc ggg	576
Leu Glu Arg Arg Lys Arg Ser Val Ala Gln Ala Thr Ser Ser Ser Gly	
180 185 190	
gag gcc cct gac agc atc aca tgg aag cca tat gat gca gcc gac ctg	624
Glu Ala Pro Asp Ser Ile Thr Trp Lys Pro Tyr Asp Ala Ala Asp Leu	
195 200 205	
gac ccc acc gag aac ccc ttc gac ctg ctt gac ttc aac cag acg cag	672
Asp Pro Thr Glu Asn Pro Phe Asp Leu Leu Asp Phe Asn Gln Thr Gln	
210 215 220	
cct gag agg ggc gac aac aac ctc acc agg atc gtg gga ggc cag gaa	720
Pro Glu Arg Gly Asp Asn Asn Leu Thr Arg Ile Val Gly Gly Gln Glu	
225 230 235 240	
tgc aag gac ggg gag tgt ccc tgg cag gcc ctg ctc atc aat gag gaa	768
Cys Lys Asp Gly Glu Cys Pro Trp Gln Ala Leu Leu Ile Asn Glu Glu	
245 250 255	
aac gag ggt ttc tgt ggt gga act att ctg agc gag ttc tac atc cta	816
Asn Glu Gly Phe Cys Gly Gly Thr Ile Leu Ser Glu Phe Tyr Ile Leu	
260 265 270	
acg gca gcc cac tgt ctc tac caa gcc aag aga ttc aag gtg agg gta	864
Thr Ala Ala His Cys Leu Tyr Gln Ala Lys Arg Phe Lys Val Arg Val	
275 280 285	
ggg gac cgg aac acg gag cag gag gag ggc ggt gag gcg gtg cac gag	912
Gly Asp Arg Asn Thr Glu Gln Glu Glu Gly Gly Glu Ala Val His Glu	
290 295 300	
gtg gag gtg gtc atc aag cac aac cgg ttc aca aag gag acc tat gac	960
Val Glu Val Val Ile Lys His Asn Arg Phe Thr Lys Glu Thr Tyr Asp	
305 310 315 320	
ttc gac atc gcc gtg ctc cgg ctc aag acc ccc atc acc ttc cgc atg	1008
Phe Asp Ile Ala Val Leu Arg Leu Lys Thr Pro Ile Thr Phe Arg Met	
325 330 335	
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Asn Val Ala Pro Ala Cys Leu Pro Glu Arg Asp Trp Ala Glu Ser Thr	
340 345 350	

ctg	atg	acg	cag	aag	acg	ggg	att	gtg	agc	ggc	ttc	ggg	cgc	acc	cac	1104
Leu	Met	Thr	Gln	Lys	Thr	Gly	Ile	Val	Ser	Gly	Phe	Gly	Arg	Thr	His	
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gag	aag	ggc	cgg	cag	tcc	acc	agg	ctc	aag	atg	ctg	gag	gtg	ccc	tac	1152
Glu	Lys	Gly	Arg	Gln	Ser	Thr	Arg	Leu	Lys	Met	Leu	Glu	Val	Pro	Tyr	
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gtg	gac	cgc	aac	agc	tgc	aag	ctg	tcc	agc	agc	ttc	atc	atc	acc	cag	1200
Val	Asp	Arg	Asn	Ser	Cys	Lys	Leu	Ser	Ser	Ser	Phe	Ile	Ile	Thr	Gln	
		385				390				395				400		
aac	atg	ttc	tgt	gcc	ggc	tac	gac	acc	aag	cag	gag	gat	gcc	tgc	cag	1248
Asn	Met	Phe	Cys	Ala	Gly	Tyr	Asp	Thr	Lys	Gln	Glu	Asp	Ala	Cys	Gln	
				405				410						415		
ggg	gac	agc	ggg	ggc	ccg	cac	gtc	acc	cgc	ttc	aag	gac	acc	tac	ttc	1296
Gly	Asp	Ser	Gly	Gly	Pro	His	Val	Thr	Arg	Phe	Lys	Asp	Thr	Tyr	Phe	
		420				425				430						
gtg	aca	ggc	atc	gtc	agc	tgg	gga	gag	agc	tgt	gcc	cgt	aag	ggg	aag	1344
Val	Thr	Gly	Ile	Val	Ser	Trp	Gly	Glu	Ser	Cys	Ala	Arg	Lys	Gly	Lys	
		435				440				445						
tac	ggg	atc	tac	acc	aag	gtc	acc	gcc	ttc	ctc	aag	tgg	atc	gac	agg	1392
Tyr	Gly	Ile	Tyr	Thr	Lys	Val	Thr	Ala	Phe	Leu	Lys	Trp	Ile	Asp	Arg	
		450				455				460						
tcc	atg	aaa	acc	agg	ggc	ttg	ccc	aag	gcc	aag	agc	cat	gcc	ccg	gag	1440
Ser	Met	Lys	Thr	Arg	Gly	Leu	Pro	Lys	Ala	Lys	Ser	His	Ala	Pro	Glu	
		465				470				475				480		
gtc	ata	acg	tcc	tct	cca	tta	aag	tga								1467
Val	Ile	Thr	Ser	Ser	Pro	Leu	Lys									
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<223> factor X
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			20					25					30		
Asn	Ile	Leu	Ala	Arg	Val	Thr	Arg	Ala	Asn	Ser	Phe	Leu	Glu	Glu	Met
		35					40					45			
Lys	Lys	Gly	His	Leu	Glu	Arg	Glu	Cys	Met	Glu	Glu	Thr	Cys	Ser	Tyr
	50					55					60				
Glu	Glu	Ala	Arg	Glu	Val	Phe	Glu	Asp	Ser	Asp	Lys	Thr	Asn	Glu	Phe
65					70					75				80	
Trp	Asn	Lys	Tyr	Lys	Asp	Gly	Asp	Gln	Cys	Glu	Thr	Ser	Pro	Cys	Gln
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Asn	Gln	Gly	Lys	Cys	Lys	Asp	Gly	Leu	Gly	Glu	Tyr	Thr	Cys	Thr	Cys
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Leu Glu Gly Phe Glu Gly Lys Asn Cys Glu Leu Phe Thr Arg Lys Leu
 115 120 125
 Cys Ser Leu Asp Asn Gly Asp Cys Asp Gln Phe Cys His Glu Glu Gln
 130 135 140
 Asn Ser Val Val Cys Ser Cys Ala Arg Gly Tyr Thr Leu Ala Asp Asn
 145 150 155 160
 Gly Lys Ala Cys Ile Pro Thr Gly Pro Tyr Pro Cys Gly Lys Gln Thr
 165 170 175
 Leu Glu Arg Arg Lys Arg Ser Val Ala Gln Ala Thr Ser Ser Ser Gly
 180 185 190
 Glu Ala Pro Asp Ser Ile Thr Trp Lys Pro Tyr Asp Ala Ala Asp Leu
 195 200 205
 Asp Pro Thr Glu Asn Pro Phe Asp Leu Leu Asp Phe Asn Gln Thr Gln
 210 215 220
 Pro Glu Arg Gly Asp Asn Asn Leu Thr Arg Ile Val Gly Gly Gln Glu
 225 230 235 240
 Cys Lys Asp Gly Glu Cys Pro Trp Gln Ala Leu Leu Ile Asn Glu Glu
 245 250 255
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 260 265 270
 Thr Ala Ala His Cys Leu Tyr Gln Ala Lys Arg Phe Lys Val Arg Val
 275 280 285
 Gly Asp Arg Asn Thr Glu Gln Glu Glu Gly Gly Glu Ala Val His Glu
 290 295 300
 Val Glu Val Val Ile Lys His Asn Arg Phe Thr Lys Glu Thr Tyr Asp
 305 310 315 320
 Phe Asp Ile Ala Val Leu Arg Leu Lys Thr Pro Ile Thr Phe Arg Met
 325 330 335
 Asn Val Ala Pro Ala Cys Leu Pro Glu Arg Asp Trp Ala Glu Ser Thr
 340 345 350
 Leu Met Thr Gln Lys Thr Gly Ile Val Ser Gly Phe Gly Arg Thr His
 355 360 365
 Glu Lys Gly Arg Gln Ser Thr Arg Leu Lys Met Leu Glu Val Pro Tyr
 370 375 380
 Val Asp Arg Asn Ser Cys Lys Leu Ser Ser Ser Phe Ile Ile Thr Gln
 385 390 395 400
 Asn Met Phe Cys Ala Gly Tyr Asp Thr Lys Gln Glu Asp Ala Cys Gln
 405 410 415
 Gly Asp Ser Gly Gly Pro His Val Thr Arg Phe Lys Asp Thr Tyr Phe
 420 425 430
 Val Thr Gly Ile Val Ser Trp Gly Glu Ser Cys Ala Arg Lys Gly Lys
 435 440 445
 Tyr Gly Ile Tyr Thr Lys Val Thr Ala Phe Leu Lys Trp Ile Asp Arg
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:PCR 5' primer
oligonucleotide #2911

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<210> 5
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<210> 6
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 oligonucleotide #5039

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<210> 7
 <211> 12
 <212> PRT
 <213> Artificial Sequence

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 protease cutting site in the region of the
 activation peptide

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<210> 8
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 <212> PRT
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<223> Description of Artificial Sequence:factor X
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activation peptide

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<210> 9

<211> 12

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:factor X analog
fX/fXIa(Q-R/I) protease cutting site in the region
of the activation peptide

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Gln Ser Phe Asn Asp Phe Thr Arg Ile Val Gly Gly
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<210> 10

<211> 10

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:factor X region
of amino acids 226-234

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<210> 11

<211> 10

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:factor X analog
modified in the activation peptide

<400> 11

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<210> 12

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:factor X analog
modified in the activation peptide

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<210> 13

<211> 10

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:factor X analog
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<210> 14

<211> 10

<212> PRT

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<223> Description of Artificial Sequence:factor X analog
modified in the activation peptide

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<210> 15

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:factor X
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<210> 16

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Q-R/I

<400> 16

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<210> 17
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<212> PRT
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<223> Description of Artificial Sequence:factor X analog
modification in the region of amino acids 227-233

<400> 17
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<210> 18
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<212> PRT
<213> Artificial Sequence

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modification in the region of amino acids 227-233

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